SEQUENCE LISTING

<110> Fox Chase Cancer Center
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Lee, Kun
Belinsky, Martin G.
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<120> MRP-Related ABC Transporter Encoding
Nucleic Acids and Methods of Use Thereof

<130> FCCC 98-02

<140> 09/647,140
<141> 2001-05-21

<150> PCT/US99/06644
<151> 1999-03-26

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Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His
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Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr
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<212> PRT
<213> Homo sapiens

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Ala Leu Glu Thr Ala Ala Arg Ala Glu Gly Leu Ser Leu Asp Ala Ser
    50   55   60
Met His Ser Gln Leu Arg Ile Leu Asp Glu Glu His Pro Lys Gly Lys
65   70   75   80
Tyr His His Gly Leu Ser Ala Leu Lys Pro Ile Arg Thr Thr Ser Lys
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His Gln His Pro Val Asp Asn Ala Gly Leu Phe Ser Cys Met Thr Phe
            100   105   110
Ser Trp Leu Ser Ser Leu Ala Arg Val Ala His Lys Lys Gly Glu Leu
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Ser Met Glu Asp Val Trp Ser Leu Ser Lys His Glu Ser Ser Asp Val
        130   135   140
Asn Cys Arg Arg Leu Glu Arg Leu Trp Gln Glu Glu Leu Asn Glu Val
145   150   155   160
Gly Pro Asp Ala Ala Ser Leu Arg Arg Val Val Trp Ile Phe Cys Arg
                165   170   175
Thr Arg Leu Ile Leu Ser Ile Val Cys Leu Met Ile Thr Gln Leu Ala
            180   185   190
Gly Phe Ser Gly Pro Ala Phe Met Val Lys His Leu Leu Glu Tyr Thr
        195   200   205
Gln Ala Thr Glu Ser Asn Leu Gln Tyr Ser Leu Leu Leu Val Leu Gly
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Leu Leu Leu Thr Glu Ile Val Arg Ser Trp Ser Leu Ala Leu Thr Trp
225   230   235   240
Ala Leu Asn Tyr Arg Thr Gly Val Arg Leu Arg Gly Ala Ile Leu Thr
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Met Ala Phe Lys Lys Ile Leu Lys Leu Lys Asn Ile Lys Glu Lys Ser
            260   265   270
Leu Gly Glu Leu Ile Asn Ile Cys Ser Asn Asp Gly Gln Arg Met Phe
        275   280   285
Glu Ala Ala Ala Val Gly Ser Leu Leu Ala Gly Gly Pro Val Val Ala
    290   295   300
Ile Leu Gly Met Ile Tyr Asn Val Ile Ile Leu Gly Pro Thr Gly Phe
305   310   315   320
Leu Gly Ser Ala Val Phe Ile Leu Phe Tyr Pro Ala Met Met Phe Ala
            325   330   335
Ser Arg Leu Thr Ala Tyr Phe Arg Arg Lys Cys Val Ala Ala Thr Asp
            340   345   350
Glu Arg Val Gln Lys Met Asn Glu Val Leu Thr Tyr Ile Lys Phe Ile
        355   360   365
Lys Met Tyr Ala Trp Val Lys Ala Phe Ser Gln Ser Val Gln Lys Ile
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Arg Glu Glu Glu Arg Arg Ile Leu Glu Lys Ala Gly Tyr Phe Gln Gly
385   390   395   400
Ile Thr Val Gly Val Ala Pro Ile Val Val Val Ile Ala Ser Val Val
                405   410   415
Thr Phe Ser Val His Met Thr Leu Gly Phe Asp Leu Thr Ala Ala Gln
            420   425   430
Ala Phe Thr Val Val Thr Val Phe Asn Ser Met Thr Phe Ala Leu Lys
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Val Thr Pro Phe Ser Val Lys Ser Leu Ser Glu Ala Ser Val Ala Val
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Leu Ala Trp Asp Ser Ser His Ser Ser Ile Gln Asn Ser Pro Lys Leu
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Thr Pro Lys Met Lys Lys Asp Lys Arg Ala Ser Arg Gly Lys Lys Glu
        515             520             525
Lys Val Arg Gln Leu Gln Arg Thr Glu His Gln Ala Val Leu Ala Glu
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Gln Lys Gly His Leu Leu Leu Asp Ser Asp Glu Arg Pro Ser Pro Glu
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Glu Glu Glu Gly Lys His Ile His Leu Gly His Leu Arg Leu Gln Arg
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Thr Leu His Ser Ile Asp Leu Glu Ile Gln Glu Gly Lys Leu Val Gly
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Ile Cys Gly Ser Val Gly Ser Gly Lys Thr Ser Leu Ile Ser Ala Ile
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Leu Gly Gln Met Thr Leu Leu Glu Gly Ser Ile Ala Ile Ser Gly Thr
610             615             620
Phe Ala Tyr Val Ala Gln Gln Ala Trp Ile Leu Asn Ala Thr Leu Arg
625             630             635             640
Asp Asn Ile Leu Phe Gly Lys Glu Tyr Asp Glu Glu Arg Tyr Asn Ser
            645             650             655
Val Leu Asn Ser Cys Cys Leu Arg Pro Asp Leu Ala Ile Leu Pro Ser
            660             665             670
Ser Asp Leu Thr Glu Ile Gly Glu Arg Gly Ala Asn Leu Ser Gly Gly
        675             680             685
Gln Arg Gln Arg Ile Ser Leu Ala Arg Ala Leu Tyr Ser Asp Arg Ser
    690             695             700
Ile Tyr Ile Leu Asp Asp Pro Leu Ser Ala Leu Asp Ala His Val Gly
705             710             715             720
Asn His Ile Phe Asn Ser Ala Ile Arg Lys His Leu Lys Ser Lys Thr
            725             730             735
Val Leu Phe Val Thr His Gln Leu Gln Tyr Leu Val Asp Cys Asp Glu
            740             745             750
Val Ile Phe Met Lys Glu Gly Cys Ile Thr Glu Arg Gly Thr His Glu
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Glu Leu Met Asn Leu Asn Gly Asp Tyr Ala Thr Ile Phe Asn Asn Leu
770             775             780
Leu Leu Gly Glu Thr Pro Pro Val Glu Ile Asn Ser Lys Lys Glu Thr
785             790             795             800
Ser Gly Ser Gln Lys Lys Ser Gln Asp Lys Gly Pro Lys Thr Gly Ser
            805             810             815
Val Lys Lys Glu Lys Ala Val Lys Pro Glu Glu Gly Gln Leu Val Gln
        820             825             830
Leu Glu Glu Lys Gly Gln Gly Ser Val Pro Trp Ser Val Tyr Gly Val
    835             840             845
Tyr Ile Gln Ala Ala Gly Gly Pro Leu Ala Phe Leu Val Ile Met Ala
    850             855             860
Leu Phe Met Leu Asn Val Gly Ser Thr Ala Phe Ser Thr Trp Trp Leu
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Ser Tyr Trp Ile Lys Gln Gly Ser Gly Asn Thr Thr Val Thr Arg Gly
            885             890             895
Asn Glu Thr Ser Val Ser Asp Ser Met Lys Asp Asn Pro His Met Gln
        900             905             910
Tyr Tyr Ala Ser Ile Tyr Ala Leu Ser Met Ala Val Met Leu Ile Leu
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Lys Ala Ile Arg Gly Val Val Phe Val Lys Gly Thr Leu Arg Ala Ser
    930             935             940
Ser Arg Leu His Asp Glu Leu Phe Arg Arg Ile Leu Arg Ser Pro Met
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Lys Phe Phe Asp Thr Thr Pro Thr Gly Arg Ile Leu Asn Arg Phe Ser
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Lys Asp Met Asp Glu Val Asp Val Arg Leu Pro Phe Gln Ala Glu Met
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Phe Ile Gln Asn Val Ile Leu Val Phe Phe Cys Val Gly Met Ile Ala
          995                1000                1005
Gly Val Phe Pro Trp Phe Leu Val Ala Val Gly Pro Leu Val Ile Leu
         1010                1015                1020
Phe Ser Val Leu His Ile Val Ser Arg Val Leu Ile Arg Glu Leu Lys
1025                1030                1035                1040
Arg Leu Asp Asn Ile Thr Gln Ser Pro Phe Leu Ser His Ile Thr Ser
                 1045                1050                1055
Ser Ile Gln Gly Leu Ala Thr Ile His Ala Tyr Asn Lys Gly Gln Glu
                 1060                1065                1070
Phe Leu His Arg Tyr Gln Glu Leu Leu Asp Asp Asn Gln Ala Pro Phe
                 1075                1080                1085
Phe Leu Phe Thr Cys Ala Met Arg Trp Leu Ala Val Arg Leu Asp Leu
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Ile Ser Ile Ala Leu Ile Thr Thr Thr Gly Leu Met Ile Val Leu Met
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His Gly Gln Ile Pro Pro Ala Tyr Ala Gly Leu Ala Ile Ser Tyr Ala
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Val Gln Leu Thr Gly Leu Phe Gln Phe Thr Val Arg Leu Ala Ser Glu
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Thr Glu Ala Arg Phe Thr Ser Val Glu Arg Ile Asn His Tyr Ile Lys
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Thr Leu Ser Leu Glu Ala Pro Ala Arg Ile Lys Asn Lys Ala Pro Ser
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Arg Tyr Arg Glu Asn Leu Pro Leu Val Leu Lys Lys Val Ser Phe Thr
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Ile Lys Pro Lys Glu Lys Ile Gly Ile Val Gly Arg Thr Gly Ser Gly
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Lys Ser Ser Leu Gly Met Ala Leu Phe Arg Leu Val Glu Leu Ser Gly
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Ser Gly Thr Val Arg Ser Asn Leu Asp Pro Phe Asn Gln Tyr Thr Glu
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Asp Gln Ile Trp Asp Ala Leu Glu Arg Thr His Met Lys Glu Cys Ile
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Asp Thr Glu Thr Asp Leu Leu Ile Gln Glu Thr Ile Arg Glu Ala Phe
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Ala Asp Cys Thr Met Leu Thr Ile Ala His Arg Leu His Thr Val Leu
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Gly Ser Asp Arg Ile Met Val Leu Ala Gln Gly Gln Val Val Glu Phe
                 1395                1400                1405
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<212> PRT
<213> Homo sapiens

<400> 6

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Gln Asn Ser Leu Leu Ala Trp Val Pro Cys Ile Tyr Leu Trp Val Ala
            35                  40                  45
Leu Pro Cys Tyr Leu Leu Tyr Leu Arg His His Cys Arg Gly Tyr Ile
        50                  55                  60
Ile Leu Ser His Leu Ser Lys Leu Lys Met Val Leu Gly Val Leu Leu
65                  70                  75                  80
Trp Cys Val Ser Trp Ala Asp Leu Phe Tyr Ser Phe His Gly Leu Val
                85                  90                  95
His Gly Arg Ala Pro Ala Pro Val Phe Phe Val Thr Pro Leu Val Val
            100                 105                 110
Gly Val Thr Met Leu Leu Ala Thr Leu Leu Ile Gln Tyr Glu Arg Leu
        115                 120                 125
Gln Gly Val Gln Ser Ser Gly Val Leu Ile Ile Phe Trp Phe Leu Cys
        130                 135                 140
Val Val Cys Ala Ile Val Pro Phe Arg Ser Lys Ile Leu Leu Ala Lys
145                 150                 155                 160
Ala Glu Gly Glu Ile Ser Asp Pro Phe Arg Phe Thr Thr Phe Tyr Ile
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His Phe Ala Leu Val Leu Ser Ala Leu Ile Leu Ala Cys Phe Arg Glu
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Lys Pro Pro Phe Phe Ser Ala Lys Asn Val Asp Pro Asn Pro Tyr Pro
        195                 200                 205
Glu Thr Ser Val Gly Phe Leu Ser Arg Leu Phe Phe Trp Trp Phe Thr
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Lys Met Ala Ile Tyr Gly Tyr Arg His Pro Leu Glu Glu Lys Asp Leu
225                 230                 235                 240
Trp Ser Leu Lys Glu Glu Asp Arg Ser Gln Met Val Val Gln Gln Leu
                245                 250                 255
Leu Glu Ala Trp Arg Lys Gln Glu Lys Gln Thr Ala Arg His Lys Ala
            260                 265                 270
Ser Ala Ala Pro Gly Lys Asn Ala Ser Gly Glu Asp Glu Val Leu Leu
        275                 280                 285
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Gln Asp Leu Leu Ser Phe Ile Asn Pro Gln Leu Leu Ser Ile Leu Ile
                325             330             335
Arg Phe Ile Ser Asn Pro Met Ala Pro Ser Trp Trp Gly Phe Leu Val
            340             345             350
Ala Gly Leu Met Phe Leu Cys Ser Met Met Gln Ser Leu Ile Leu Gln
        355             360             365
His Tyr Tyr His Tyr Ile Phe Val Thr Gly Val Lys Phe Arg Thr Gly
    370             375             380
Ile Met Gly Val Ile Tyr Arg Lys Ala Leu Val Ile Thr Asn Ser Val
385             390             395                 400
Lys Arg Ala Ser Thr Val Gly Glu Ile Val Asn Leu Met Ser Val Asp
            405             410             415
Ala Gln Arg Phe Met Asp Leu Ala Pro Phe Leu Asn Leu Leu Trp Ser
        420             425             430
Ala Pro Leu Gln Ile Ile Leu Ala Ile Tyr Phe Leu Trp Gln Asn Leu
        435             440             445
Gly Pro Ser Val Leu Ala Gly Val Ala Phe Met Val Leu Leu Ile Pro
    450             455             460
Leu Asn Gly Ala Val Ala Val Lys Met Arg Ala Phe Gln Val Lys Gln
465             470             475                 480
Met Lys Leu Lys Asp Ser Arg Ile Lys Leu Met Ser Glu Ile Leu Asn
            485             490             495
Gly Ile Lys Val Leu Lys Leu Tyr Ala Trp Glu Pro Ser Phe Leu Lys
        500             505             510
Gln Val Glu Gly Ile Arg Gln Gly Glu Leu Gln Leu Leu Arg Thr Ala
        515             520             525
Ala Tyr Leu His Thr Thr Thr Thr Phe Thr Trp Met Cys Ser Pro Phe
    530             535             540
Leu Val Thr Leu Ile Thr Leu Trp Val Tyr Val Tyr Val Asp Pro Asn
545             550             555                 560
Asn Val Leu Asp Ala Glu Lys Ala Phe Val Ser Val Ser Leu Phe Asn
            565             570             575
Ile Leu Arg Leu Pro Leu Asn Met Leu Pro Gln Leu Ile Ser Asn Leu
            580             585             590
Thr Gln Ala Ser Val Ser Leu Lys Arg Ile Gln Gln Phe Leu Ser Gln
        595             600             605
Glu Glu Leu Asp Pro Gln Ser Val Glu Arg Lys Thr Ile Ser Pro Gly
    610             615             620
Tyr Ala Ile Thr Ile His Ser Gly Thr Phe Thr Trp Ala Gln Asp Leu
625             630             635                 640
Pro Pro Thr Leu His Ser Leu Asp Ile Gln Val Pro Lys Gly Ala Leu
            645             650             655
Val Ala Val Val Gly Pro Val Gly Cys Gly Lys Ser Ser Leu Val Ser
            660             665             670
Ala Leu Leu Gly Glu Met Glu Lys Leu Glu Gly Lys Val His Met Lys
        675             680             685
Gly Ser Val Ala Tyr Val Pro Gln Gln Ala Trp Ile Gln Asn Cys Thr
    690             695             700
Leu Gln Glu Asn Val Leu Phe Gly Lys Ala Leu Asn Pro Lys Arg Tyr
705             710             715                 720
Gln Gln Thr Leu Glu Ala Cys Ala Leu Leu Ala Asp Leu Glu Met Leu
            725             730             735
Pro Gly Gly Asp Gln Thr Glu Ile Gly Glu Lys Gly Ile Asn Leu Ser
            740             745             750
Gly Gly Gln Arg Gln Arg Val Ser Leu Ala Arg Ala Val Tyr Ser Asp
        755             760             765
Ala Asp Ile Phe Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ser His
    770             775             780
Val Ala Lys His Ile Phe Asp His Val Ile Gly Pro Glu Gly Val Leu
785             790             795                 800
```

```
Ala Gly Lys Thr Arg Val Leu Val Thr His Gly Ile Ser Phe Leu Pro
            805                     810                 815
Gln Thr Asp Phe Ile Ile Val Leu Ala Asp Gly Gln Val Ser Glu Met
            820                     825                 830
Gly Pro Tyr Pro Ala Leu Leu Gln Arg Asn Gly Ser Phe Ala Asn Phe
            835                     840                 845
Leu Cys Asn Tyr Ala Pro Asp Glu Asp Gln Gly His Leu Glu Asp Ser
        850                     855                 860
Trp Thr Ala Leu Glu Gly Ala Glu Asp Lys Glu Ala Leu Leu Ile Glu
865                     870                     875                 880
Asp Thr Leu Ser Asn His Thr Asp Leu Thr Asp Asn Asp Pro Val Thr
            885                     890                 895
Tyr Val Val Gln Lys Gln Phe Met Arg Gln Leu Ser Ala Leu Ser Ser
            900                     905                 910
Asp Gly Glu Gly Gln Gly Arg Pro Val Pro Arg Arg His Leu Gly Pro
        915                     920                 925
Ser Glu Lys Val Gln Val Thr Glu Ala Lys Ala Asp Gly Ala Leu Thr
        930                     935                 940
Gln Glu Glu Lys Ala Ala Ile Gly Thr Val Glu Leu Ser Val Phe Trp
945                     950                     955                 960
Asp Tyr Ala Lys Ala Val Gly Leu Cys Thr Thr Leu Ala Ile Cys Leu
            965                     970                 975
Leu Tyr Val Gly Gln Ser Ala Ala Ala Ile Gly Ala Asn Val Trp Leu
            980                     985                 990
Ser Ala Trp Thr Asn Asp Ala Met Ala Asp Ser Arg Gln Asn Asn Thr
        995                     1000                1005
Ser Leu Arg Leu Gly Val Tyr Ala Ala Leu Gly Ile Leu Gln Gly Phe
        1010                    1015                1020
Leu Val Met Leu Ala Ala Met Ala Met Ala Ala Gly Gly Ile Gln Ala
1025                    1030                    1035                1040
Ala Arg Val Leu His Gln Ala Leu Leu His Asn Lys Ile Arg Ser Pro
            1045                    1050                1055
Gln Ser Phe Phe Asp Thr Thr Pro Ser Gly Arg Ile Leu Asn Cys Phe
            1060                    1065                1070
Ser Lys Asp Ile Tyr Val Val Asp Glu Val Leu Ala Pro Val Ile Leu
        1075                    1080                1085
Met Leu Leu Asn Ser Phe Phe Asn Ala Ile Ser Thr Leu Val Val Ile
        1090                    1095                1100
Met Ala Ser Thr Pro Leu Phe Thr Val Val Ile Leu Pro Leu Ala Val
1105                    1110                    1115                1120
Leu Tyr Thr Leu Val Gln Arg Phe Tyr Ala Ala Thr Ser Arg Gln Leu
            1125                    1130                1135
Lys Arg Leu Glu Ser Val Ser Arg Ser Pro Ile Tyr Ser His Phe Ser
            1140                    1145                1150
Glu Thr Val Thr Gly Ala Ser Val Ile Arg Ala Tyr Asn Arg Ser Arg
        1155                    1160                1165
Asp Phe Glu Ile Ile Ser Asp Thr Lys Val Asp Ala Asn Gln Arg Ser
        1170                    1175                1180
Cys Tyr Pro Tyr Ile Ile Ser Asn Arg Trp Leu Ser Ile Gly Val Glu
1185                    1190                    1195                1200
Phe Val Gly Asn Cys Val Val Leu Phe Ala Ala Leu Phe Ala Val Ile
            1205                    1210                1215
Gly Arg Ser Ser Leu Asn Pro Gly Leu Val Gly Leu Ser Val Ser Tyr
            1220                    1225                1230
Ser Leu Gln Val Thr Phe Ala Leu Asn Trp Met Ile Arg Met Met Ser
            1235                    1240                1245
Asp Leu Glu Ser Asn Ile Val Ala Val Glu Arg Val Lys Glu Tyr Ser
        1250                    1255                1260
Lys Thr Glu Thr Glu Ala Pro Trp Val Val Glu Gly Ser Arg Pro Pro
1265                    1270                    1275                1280
Glu Gly Trp Pro Pro Arg Gly Glu Val Glu Phe Arg Asn Tyr Ser Val
            1285                    1290                1295
Arg Tyr Arg Pro Gly Leu Asp Leu Val Leu Arg Asp Leu Ser Leu His
            1300                    1305                1310
```

```
Val His Gly Gly Glu Lys Val Gly Ile Val Gly Arg Thr Gly Ala Gly
        1315                1320                1325
Lys Ser Ser Met Thr Leu Cys Leu Phe Arg Ile Leu Glu Ala Ala Lys
    1330                1335                1340
Gly Glu Ile Arg Ile Asp Gly Leu Asn Val Ala Asp Ile Gly Leu His
1345                1350                1355                1360
Asp Leu Arg Ser Gln Leu Thr Ile Ile Pro Gln Asp Pro Ile Leu Phe
            1365                1370                1375
Ser Gly Thr Leu Arg Met Asn Leu Asp Pro Phe Gly Ser Tyr Ser Glu
            1380                1385                1390
Glu Asp Ile Trp Trp Ala Leu Glu Leu Ser His Leu His Thr Phe Val
            1395                1400                1405
Ser Ser Gln Pro Ala Gly Leu Asp Phe Gln Cys Ser Glu Gly Gly Glu
    1410                1415                1420
Asn Leu Ser Val Gly Gln Arg Gln Leu Val Cys Leu Ala Arg Ala Leu
1425                1430                1435                1440
Leu Arg Lys Ser Arg Ile Leu Val Leu Asp Glu Ala Thr Ala Ala Ile
            1445                1450                1455
Asp Leu Glu Thr Asp Asn Leu Ile Gln Ala Thr Ile Arg Thr Gln Phe
            1460                1465                1470
Asp Thr Cys Thr Val Leu Thr Ile Ala His Arg Leu Asn Thr Ile Met
    1475                1480                1485
Asp Tyr Thr Arg Val Leu Val Leu Asp Lys Gly Val Val Ala Glu Phe
    1490                1495                1500
Asp Ser Pro Ala Asn Leu Ile Ala Ala Arg Gly Ile Phe Tyr Gly Met
1505                1510                1515                1520
Ala Arg Asp Ala Gly Leu Ala
            1525


        <210> 7
        <211> 4509
        <212> DNA
        <213> Homo sapiens

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cccatgtacc tctgggtcct tggtcccatc tacctcctct tcatccacca ccatggccgg    180
ggctacctcc ggatgtcccc actcttcaaa gccaagatgg tgcttggatt cgccctcata    240
gtcctgtgta cctccagcgt ggctgtcgct ctttggaaaa tccaacaggg aacgcctgag    300
gcccccagaat tcctcattca tcctactgtg tggctcacca cgatgagctt cgcagtgttc    360
ctgattcaca ccgagaggaa aaagggagtc cagtcatctg gagtgctgtt tggttactgg    420
cttctctgct ttgtcttgcc agctaccaac gctgcccagc aggcctccgg agcgggcttc    480
cagagcgacc ctgtccgcca cctgtccacc tacctatgcc tgtctctggt ggtggcacag    540
tttgtgctgt cctgcctggc ggatcaaccc cccttcttcc ctgaagaccc ccagcagtct    600
aaccccctgtc cagagactgg ggcagccttc ccctccaaag ccacgttctg gtgggtttct    660
ggcctggtct ggaggggata caggaggcca ctgagaccaa aagacctctg gtcgcttggg    720
agagaaaaact cctcagaaga acttgtttcc cggcttgaaa aggagtggat gaggaaccgc    780
agtgcagccc ggaggcacaa caaggcaata gcatttaaaa ggaaaggcgg cagtggcatg    840
aaggctccag agaccgagcc cttcctacgg caagaaggga gccagtggcg cccactgctg    900
aaggccatct ggcaggtgtt ccattctacc ttcctcctgg ggaccctcag cctcatcatc    960
agtgatgtct tcaggttcac tgtccccaag ctgctcagcc ttttcctgga gtttattggt    1020
gatcccaagc tccagcctg gaagggctac ctcctcgccg tgctgatgtt cctctcagcc    1080
tgcctgcaaa cgctgtttga gcagcagaac atgtacaggc tcaaggtgcc gcagatgagg    1140
ttgcggtcgg ccatcactgg cctggtgtac agaaaggtcc tggctctgtc cagcggctcc    1200
agaaaggcca gtgcggtggg tgatgtggtc aatctggtgt ccgtggacgt gcagcggctg    1260
accgagagcg tcctctacct caacgggctg tggctgcctc tcgtctggat cgtggtctgc    1320
ttcgtctatc tctggcagct cctggggccc tccgccctca ctgccatcgc tgtcttcctg    1380
agcctcctcc ctctgaattt cttcatctcc aagaaaagga accaccatca ggaggagcaa    1440
atgaggcaga aggactcacg ggcacggctc accagctcta tcctcaggaa ctcgaagacc    1500
atcaagttcc atggctggga gggagccttt ctggacagag tcctgggcat ccgaggccag    1560
gagctgggcg ccttgcggac ctccggcctc ctcttctctg tgtcgctggt gtccttccaa    1620
gtgtctacat ttctggtcgc actggtggtg tttgctgtcc acactctggt ggccgagaat    1680
gctatgaatg cagagaaagc ctttgtgact ctcacagttc tcaacatcct caacaaggcc    1740
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caggctttcc tgcccttctc catccactcc ctcgtccagg cccgggtgtc ctttgaccgt      1800
ctggtcacct tcctctgcct ggaagaagtt gaccctggtg tcgtagactc aagttcctct      1860
ggaagcgctg ccgggaagga ttgcatcacc atacacagtg ccaccttcgc ctggtcccag      1920
gaaagccctc cctgcctcca cagaataaac ctcacggtgc cccagggctg tctgctggct      1980
gttgtcggtc cagtggggggc agggaagtcc tccctgctgt ccgccctcct ggggggagctg     2040
tcaaaggtgg aggggttcgt gagcatcgag ggtgctgtgg cctacgtgcc ccaggaggcc      2100
tgggtgcaga acacctctgt ggtagagaat gtgtgcttcg ggcaggagct ggacccaccc      2160
tggctggaga gagtactaga agcctgtgcc ctgcagccag atgtggacag cttccctgag      2220
ggaatccaca cttcaattgg ggagcagggc atgaatctct ccggaggcca gaagcagcgg      2280
ctgagcctgg cccgggctgt atacagaaag gcagctgtgt acctgctgga tgacccctg      2340
gcggccctgg atgcccacgt tggccagcat gtcttcaacc aggtcattgg gcctggtggg      2400
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gattggatca tagtgctggc aaatgggggc atcgcagaga tgggttccta ccaggagctt      2520
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caggcgggc agatcgagtt ccgggacttt gggctaagat gccgacctga gctcccgctg       3840
gctgtgcagg gcgtgtcctt caagatccac gcaggagaga aggtgggcat cgttggcagg      3900
accggggcag ggaagtcctc cctggccagt gggctgctgc ggctccagga ggcagctgag      3960
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gacctgctgc aggagcactc ggacgaggct atctgggcag ccctggagac ggtgcagctc      4140
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gacctgagcg tgggccagaa acagctcctg tgtctggcac gtgcccttct ccggaagacc      4260
cagatcctca tcctggacga ggctactgct gccgtggacc ctggcacgga gctgcagatg      4320
caggccatgc tcggagctg gtttgcacag tgcactgtgc tgcccattgc ccaccgcctg       4380
cgctccgtga tggactgtgc ccgggttctg gtcatggaca ggggggcaggt ggcagagagc      4440
ggcagcccgg cccagctgct ggcccagaag ggcctgtttt acagactggc ccaggagtca      4500
ggcctggtc                                                              4509


        <210> 8
        <211> 1503
        <212> PRT
        <213> Homo sapiens

        <400> 8
Met Ala Ala Pro Ala Glu Pro Cys Ala Gly Gln Gly Val Trp Asn Gln
 1               5                  10                  15
Thr Glu Pro Glu Pro Ala Ala Thr Ser Leu Leu Ser Leu Cys Phe Leu
            20                  25                  30
Arg Thr Ala Gly Val Trp Val Pro Pro Met Tyr Leu Trp Val Leu Gly
            35                  40                  45
Pro Ile Tyr Leu Leu Phe Ile His His His Gly Arg Gly Tyr Leu Arg
        50                  55                  60
Met Ser Pro Leu Phe Lys Ala Lys Met Val Leu Gly Phe Ala Leu Ile
65                  70                  75                  80
```

```
Val Leu Cys Thr Ser Ser Val Ala Val Ala Leu Trp Lys Ile Gln Gln
                    85                  90                  95
Gly Thr Pro Glu Ala Pro Glu Phe Leu Ile His Pro Thr Val Trp Leu
                100                 105                 110
Thr Thr Met Ser Phe Ala Val Phe Leu Ile His Thr Glu Arg Lys Lys
        115                 120                 125
Gly Val Gln Ser Ser Gly Val Leu Phe Gly Tyr Trp Leu Leu Cys Phe
    130                 135                 140
Val Leu Pro Ala Thr Asn Ala Ala Gln Gln Ala Ser Gly Ala Gly Phe
145                 150                 155                 160
Gln Ser Asp Pro Val Arg His Leu Ser Thr Tyr Leu Cys Leu Ser Leu
                165                 170                 175
Val Val Ala Gln Phe Val Leu Ser Cys Leu Ala Asp Gln Pro Pro Phe
            180                 185                 190
Phe Pro Glu Asp Pro Gln Gln Ser Asn Pro Cys Pro Glu Thr Gly Ala
    195                 200                 205
Ala Phe Pro Ser Lys Ala Thr Phe Trp Trp Val Ser Gly Leu Val Trp
    210                 215                 220
Arg Gly Tyr Arg Arg Pro Leu Arg Pro Lys Asp Leu Trp Ser Leu Gly
225                 230                 235                 240
Arg Glu Asn Ser Ser Glu Glu Leu Val Ser Arg Leu Glu Lys Glu Trp
                245                 250                 255
Met Arg Asn Arg Ser Ala Ala Arg Arg His Asn Lys Ala Ile Ala Phe
                260                 265                 270
Lys Arg Lys Gly Gly Ser Gly Met Lys Ala Pro Glu Thr Glu Pro Phe
        275                 280                 285
Leu Arg Gln Glu Gly Ser Gln Trp Arg Pro Leu Leu Lys Ala Ile Trp
    290                 295                 300
Gln Val Phe His Ser Thr Phe Leu Leu Gly Thr Leu Ser Leu Ile Ile
305                 310                 315                 320
Ser Asp Val Phe Arg Phe Thr Val Pro Lys Leu Leu Ser Leu Phe Leu
                325                 330                 335
Glu Phe Ile Gly Asp Pro Lys Pro Pro Ala Trp Lys Gly Tyr Leu Leu
            340                 345                 350
Ala Val Leu Met Phe Leu Ser Ala Cys Leu Gln Thr Leu Phe Glu Gln
        355                 360                 365
Gln Asn Met Tyr Arg Leu Lys Val Pro Gln Met Arg Leu Arg Ser Ala
    370                 375                 380
Ile Thr Gly Leu Val Tyr Arg Lys Val Leu Ala Leu Ser Ser Gly Ser
385                 390                 395                 400
Arg Lys Ala Ser Ala Val Gly Asp Val Val Asn Leu Val Ser Val Asp
                405                 410                 415
Val Gln Arg Leu Thr Glu Ser Val Leu Tyr Leu Asn Gly Leu Trp Leu
                420                 425                 430
Pro Leu Val Trp Ile Val Val Cys Phe Val Tyr Leu Trp Gln Leu Leu
            435                 440                 445
Gly Pro Ser Ala Leu Thr Ala Ile Ala Val Phe Leu Ser Leu Leu Pro
    450                 455                 460
Leu Asn Phe Phe Ile Ser Lys Lys Arg Asn His His Gln Glu Glu Gln
465                 470                 475                 480
Met Arg Gln Lys Asp Ser Arg Ala Arg Leu Thr Ser Ser Ile Leu Arg
                485                 490                 495
Asn Ser Lys Thr Ile Lys Phe His Gly Trp Glu Gly Ala Phe Leu Asp
                500                 505                 510
Arg Val Leu Gly Ile Arg Gly Gln Glu Leu Gly Ala Leu Arg Thr Ser
        515                 520                 525
Gly Leu Leu Phe Ser Val Ser Leu Val Ser Phe Gln Val Ser Thr Phe
    530                 535                 540
Leu Val Ala Leu Val Val Phe Ala Val His Thr Leu Val Ala Glu Asn
545                 550                 555                 560
Ala Met Asn Ala Glu Lys Ala Phe Val Thr Leu Thr Val Leu Asn Ile
            565                 570                 575
Leu Asn Lys Ala Gln Ala Phe Leu Pro Phe Ser Ile His Ser Leu Val
            580                 585                 590
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<220>
<221> misc_feature
<222> (18)...(18)
<223> n = a, c, g or t

<400> 9
ctdgtdgcdg tdgtdggn                                                    18


<210> 10
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence source:/note="synthetic construct"

<400> 10
atggccgcgc ctgctgagc                                                  19


<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence source:/note="synthetic construct"

<400> 11
gtctacgaca ccagggtcaa                                                 20


<210> 12
<211> 20
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<213> Artificial Sequence

<220>
<223> Sequence source:/note="synthetic construct"

<400> 12
ctgcctggaa gaagttgacc                                                 20


<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence source:/note="synthetic construct"

<400> 13
ctggaatgtc cacgtcaacc                                                 20


<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence source:/note="synthetic construct"
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Gln Ala Arg Val Ser Phe Asp Arg Leu Val Thr Phe Leu Cys Leu Glu
        595                 600                 605
Glu Val Asp Pro Gly Val Val Asp Ser Ser Ser Ser Gly Ser Ala Ala
    610                 615                 620
Gly Lys Asp Cys Ile Thr Ile His Ser Ala Thr Phe Ala Trp Ser Gln
625                 630                 635                 640
Glu Ser Pro Pro Cys Leu His Arg Ile Asn Leu Thr Val Pro Gln Gly
            645                 650                 655
Cys Leu Leu Ala Val Val Gly Pro Val Gly Ala Gly Lys Ser Ser Leu
        660                 665                 670
Leu Ser Ala Leu Leu Gly Glu Leu Ser Lys Val Glu Gly Phe Val Ser
        675                 680                 685
Ile Glu Gly Ala Val Ala Tyr Val Pro Gln Glu Ala Trp Val Gln Asn
    690                 695                 700
Thr Ser Val Val Glu Asn Val Cys Phe Gly Gln Glu Leu Asp Pro Pro
705                 710                 715                 720
Trp Leu Glu Arg Val Leu Glu Ala Cys Ala Leu Gln Pro Asp Val Asp
            725                 730                 735
Ser Phe Pro Glu Gly Ile His Thr Ser Ile Gly Glu Gln Gly Met Asn
            740                 745                 750
Leu Ser Gly Gly Gln Lys Gln Arg Leu Ser Leu Ala Arg Ala Val Tyr
        755                 760                 765
Arg Lys Ala Ala Val Tyr Leu Leu Asp Asp Pro Leu Ala Ala Leu Asp
        770                 775                 780
Ala His Val Gly Gln His Val Phe Asn Gln Val Ile Gly Pro Gly Gly
785                 790                 795                 800
Leu Leu Gln Gly Thr Thr Arg Ile Leu Val Thr His Ala Leu His Ile
            805                 810                 815
Leu Pro Gln Ala Asp Trp Ile Ile Val Leu Ala Asn Gly Ala Ile Ala
            820                 825                 830
Glu Met Gly Ser Tyr Gln Glu Leu Leu Gln Arg Lys Gly Ala Leu Val
        835                 840                 845
Cys Leu Leu Asp Gln Ala Arg Gln Pro Gly Asp Arg Gly Glu Gly Glu
    850                 855                 860
Thr Glu Pro Gly Thr Ser Thr Lys Asp Pro Arg Gly Thr Ser Ala Gly
865                 870                 875                 880
Arg Arg Pro Glu Leu Arg Arg Glu Arg Ser Ile Lys Ser Val Pro Glu
            885                 890                 895
Lys Asp Arg Thr Thr Ser Glu Ala Gln Thr Glu Val Pro Leu Asp Asp
        900                 905                 910
Pro Asp Arg Ala Gly Trp Pro Ala Gly Lys Asp Ser Ile Gln Tyr Gly
        915                 920                 925
Arg Val Lys Ala Thr Val His Leu Ala Tyr Leu Arg Ala Val Gly Thr
    930                 935                 940
Pro Leu Cys Leu Tyr Ala Leu Phe Leu Phe Leu Cys Gln Gln Val Ala
945                 950                 955                 960
Ser Phe Cys Arg Gly Tyr Trp Leu Ser Leu Trp Ala Asp Asp Pro Ala
            965                 970                 975
Val Gly Gly Gln Gln Thr Gln Ala Ala Leu Arg Gly Gly Ile Phe Gly
        980                 985                 990
Leu Leu Gly Cys Leu Gln Ala Ile Gly Leu Phe Ala Ser Met Ala Ala
        995                 1000                1005
Val Leu Leu Gly Gly Ala Arg Ala Ser Arg Leu Leu Phe Gln Arg Leu
    1010                1015                1020
Leu Trp Asp Val Val Arg Ser Pro Ile Ser Phe Phe Glu Arg Thr Pro
1025                1030                1035                1040
Ile Gly His Leu Leu Asn Arg Phe Ser Lys Glu Thr Asp Thr Val Asp
            1045                1050                1055
Val Asp Ile Pro Asp Lys Leu Arg Ser Leu Leu Met Tyr Ala Phe Gly
            1060                1065                1070
Leu Leu Glu Val Ser Leu Val Val Ala Val Ala Thr Pro Leu Ala Thr
        1075                1080                1085
Val Ala Ile Leu Pro Leu Phe Leu Leu Tyr Ala Gly Phe Gln Ser Leu
    1090                1095                1100
```

```
Tyr Val Val Ser Ser Cys Gln Leu Arg Arg Leu Glu Ser Ala Ser Tyr
1105                1110                1115                1120
Ser Ser Val Cys Ser His Met Ala Glu Thr Phe Gln Gly Ser Thr Val
                1125                1130                1135
Val Arg Ala Phe Arg Thr Gln Ala Pro Phe Val Ala Gln Asn Asn Ala
            1140                1145                1150
Arg Val Asp Glu Ser Gln Arg Ile Ser Phe Pro Arg Leu Val Ala Asp
        1155                1160                1165
Arg Trp Leu Ala Ala Asn Val Glu Leu Leu Gly Asn Gly Leu Val Phe
    1170                1175                1180
Ala Ala Ala Thr Cys Ala Val Leu Ser Lys Ala His Leu Ser Ala Gly
1185                1190                1195                1200
Leu Val Gly Phe Ser Val Ser Ala Ala Leu Gln Val Thr Gln Ala Leu
                1205                1210                1215
Gln Trp Val Val Arg Asn Trp Thr Asp Leu Glu Asn Ser Ile Val Ser
            1220                1225                1230
Val Glu Arg Met Gln Asp Tyr Ala Trp Thr Pro Lys Glu Ala Pro Trp
        1235                1240                1245
Arg Leu Pro Thr Cys Ala Ala Gln Pro Pro Trp Pro Gln Gly Gly Gln
    1250                1255                1260
Ile Glu Phe Arg Asp Phe Gly Leu Arg Tyr Arg Pro Glu Leu Pro Leu
1265                1270                1275                1280
Ala Val Gln Gly Val Ser Leu Lys Ile His Ala Gly Glu Lys Val Gly
                1285                1290                1295
Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Ala Ser Gly Leu
                1300                1305                1310
Leu Arg Leu Gln Glu Ala Ala Glu Gly Gly Ile Trp Ile Asp Gly Val
            1315                1320                1325
Pro Ile Ala His Val Gly Leu His Thr Leu Arg Ser Arg Ile Ser Ile
        1330                1335                1340
Ile Pro Gln Asp Pro Ile Leu Phe Pro Gly Ser Leu Arg Met Asn Leu
1345                1350                1355                1360
Asp Leu Leu Gln Glu His Ser Asp Glu Ala Ile Trp Ala Ala Leu Glu
                1365                1370                1375
Thr Val Gln Leu Lys Ala Leu Val Ala Ser Leu Pro Gly Gln Leu Gln
            1380                1385                1390
Tyr Lys Cys Ala Asp Arg Gly Glu Asp Leu Ser Val Gly Gln Lys Gln
        1395                1400                1405
Leu Leu Cys Leu Ala Arg Ala Leu Leu Arg Lys Thr Gln Ile Leu Ile
    1410                1415                1420
Leu Asp Glu Ala Thr Ala Ala Val Asp Pro Gly Thr Glu Leu Gln Met
1425                1430                1435                1440
Gln Ala Met Leu Gly Ser Trp Phe Ala Gln Cys Thr Val Leu Leu Ile
                1445                1450                1455
Ala His Arg Leu Arg Ser Val Met Asp Cys Ala Arg Val Leu Val Met
            1460                1465                1470
Asp Lys Gly Gln Val Ala Glu Ser Gly Ser Pro Ala Gln Leu Leu Ala
        1475                1480                1485
Gln Lys Gly Leu Phe Tyr Arg Leu Ala Gln Glu Ser Gly Leu Val
    1490                1495                1500


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        <211> 18
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Sequence source:/note="synthetic construct"

        <220>
        <221> misc_feature
        <222> (3)...(15)
        <223> d = a, g or t
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ggagacagac acggttgacg                                              20


      <210> 15
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      <212> DNA
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      <220>
      <223> Sequence source:/note="synthetic construct"

      <400> 15
gcagaccagg cctgactcc                                               19


      <210> 16
      <211> 24
      <212> DNA
      <213> Artificial Sequence

      <220>
      <223> Sequence source:/note="synthetic construct"

      <220>
      <221> misc_feature
      <222> (1)...(22)
      <223> r = a or g

      <220>
      <221> misc_feature
      <222> (4)...(19)
      <223> n = a, c, g or t

      <220>
      <221> misc_feature
      <222> (6)...(6)
      <223> v = a, c or g

      <220>
      <221> misc_feature
      <222> (11)...(11)
      <223> s = c or g

      <220>
      <221> misc_feature
      <222> (12)...(12)
      <223> w = a or t

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rctnavngcn swnarnggnt crtc                                         24


      <210> 17
      <211> 29
      <212> DNA
      <213> Artificial Sequence

      <220>
      <223> Sequence source:/note="synthetic construct"

      <220>
      <221> misc_feature
      <222> (11)...(14)
      <223> r = a or g
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<221> misc_feature
<222> (17)...(17)
<223> y = c or t

<220>
<221> misc_feature
<222> (20)...(20)
<223> h = a, c or t

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<222> (23)...(29)
<223> n = a, c, g or t

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cgggatccag rgaraayath ctntttggn                                    29


<210> 18
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<220>
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<220>
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<222> (12)...(27)
<223> r = a or g

<220>
<221> misc_feature
<222> (15)...(15)
<223> h = a, c or t

<220>
<221> misc_feature
<222> (24)...(24)
<223> d = a, g or t

<400> 18
cggaattcnt crtchagnag rtadatrtc                                    29
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